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RAW SEQUENCE LISTING

DATE: 08/28/2001

PATENT APPLICATION: US/09/837,235

TIME: 10:22:38

Input Set : A:\9725-005-999.txt

Output Set: N:\CRF3\08282001\I837235.raw

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5 <110> APPLICANT: Marshall, Christopher
7 Hoffman, Alexander
9 Errico, Joseph
11 Marshall, Paul
15 <120> TITLE OF INVENTION: STABILIZED PROTEINS
19 <130> FILE REFERENCE: 9725-005-999
23 <140> CURRENT APPLICATION NUMBER: 09/837,235
25 <141> CURRENT FILING DATE: 2001-04-18
29 <150> PRIOR APPLICATION NUMBER: PCT/US00/28595
31 <151> PRIOR FILING DATE: 2000-10-16
35 <150> PRIOR APPLICATION NUMBER: 60/159,763
37 <151> PRIOR FILING DATE: 1999-10-15
41 <160> NUMBER OF SEQ ID NOS: 42
45 <170> SOFTWARE: PatentIn version 3.0
49 <210> SEQ ID NO: 1
51 <211> LENGTH: 954
53 <212> TYPE: DNA
55 <213> ORGANISM: Candida antarctica
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62 acctgccagg gtgcttcgcc atcctcggtc tccaaacca tccttctcgt ccccggaacc 120
64 ggcaccacag gtccacagtc gttcgactcg aactggatcc ccctctcaac gcagttgggt 180
66 tacacaccct gctggatctc acccccgccg ttcatgctca acgacacca ggtcaacacg 240
68 gagtacatgg tcaacgccat caccgcgctc tacgttggtt cgggcaacaa caagcttccc 300
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80 tcatcctacc tcttcaacgg aaagaacgtc caggcacagg ccgtgtgtgg gccgctgttc 660
82 gtcacgacc atgcaggctc gctcacctcg cagttctcct acgtcgtcgg tcgatccgcc 720
84 ctgcgctcca ccacgggcca ggctcgtagt gcagactatg gcattacgga ctgcaaccct 780
86 cttcccgcca atgatctgac tcccgagcaa aaggctgccg cggctgcgct cctggcgccg 840
88 gcagctgcag ccacgtggc ggggtccaaag cagaactgcg agcccgaact catgccctac 900
90 gcccgccctt ttgcagtagg caaaaggacc tgctccggca tcgtcaccct ctga 954
93 <210> SEQ ID NO: 2
95 <211> LENGTH: 317
97 <212> TYPE: PRT
99 <213> ORGANISM: Candida antarctica
103 <400> SEQUENCE: 2
105 Leu Pro Ser Gly Ser Asp Pro Ala Phe Ser Gln Pro Lys Ser Val Leu
106 1 5 10 15
108 Asp Ala Gly Leu Thr Cys Gln Gly Ala Ser Pro Ser Ser Val Ser Lys
109 20 25 30
111 Pro Ile Leu Leu Val Pro Gly Thr Gly Thr Thr Gly Pro Gln Ser Phe
112 35 40 45
114 Asp Ser Asn Trp Ile Pro Leu Ser Thr Gln Leu Gly Tyr Thr Pro Cys

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115      50                      55                      60
117 Trp Ile Ser Pro Pro Pro Phe Met Leu Asn Asp Thr Gln Val Asn Thr
118 65                      70                      75                      80
120 Glu Tyr Met Val Asn Ala Ile Thr Ala Leu Tyr Ala Gly Ser Gly Asn
121                      85                      90                      95
123 Asn Lys Leu Pro Val Leu Thr Trp Ser Gln Gly Gly Leu Val Ala Gln
124                      100                      105                      110
126 Trp Gly Leu Thr Phe Phe Pro Ser Ile Arg Ser Lys Val Asp Arg Leu
127                      115                      120                      125
129 Met Ala Phe Ala Pro Asp Tyr Lys Gly Thr Val Leu Ala Gly Pro Leu
130                      130                      135                      140
132 Asp Ala Leu Ala Val Ser Ala Pro Ser Val Trp Gln Gln Thr Thr Gly
133 145                      150                      155                      160
135 Ser Ala Leu Thr Thr Ala Leu Arg Asn Ala Gly Gly Leu Thr Gln Ile
136                      165                      170                      175
138 Val Pro Thr Thr Asn Leu Tyr Ser Ala Thr Asp Glu Ile Val Gln Pro
139                      180                      185                      190
141 Gln Val Ser Asn Ser Pro Leu Asp Ser Ser Tyr Leu Phe Asn Gly Lys
142                      195                      200                      205
144 Asn Val Gln Ala Gln Ala Val Cys Gly Pro Leu Phe Val Ile Asp His
145                      210                      215                      220
147 Ala Gly Ser Leu Thr Ser Gln Phe Ser Tyr Val Val Gly Arg Ser Ala
148 225                      230                      235                      240
150 Leu Arg Ser Thr Thr Gly Gln Ala Arg Ser Ala Asp Tyr Gly Ile Thr
151                      245                      250                      255
153 Asp Cys Asn Pro Leu Pro Ala Asn Asp Leu Thr Pro Glu Gln Lys Val
154                      260                      265                      270
156 Ala Ala Ala Ala Leu Leu Ala Pro Ala Ala Ala Ala Ile Val Ala Gly
157                      275                      280                      285
159 Pro Lys Gln Asn Cys Glu Pro Asp Leu Met Pro Tyr Ala Arg Pro Phe
160                      290                      295                      300
162 Ala Val Gly Lys Arg Thr Cys Ser Gly Ile Val Thr Pro
163 305                      310                      315

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165 <210> SEQ ID NO: 3

167 <211> LENGTH: 57

169 <212> TYPE: DNA

171 <213> ORGANISM: Candida antarctica

175 <400> SEQUENCE: 3

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57

179 <210> SEQ ID NO: 4

181 <211> LENGTH: 37

183 <212> TYPE: DNA

185 <213> ORGANISM: Candida antarctica

189 <400> SEQUENCE: 4

190 ctcttggcgg ccgcctatca gggggtgacg atgccgg

37

193 <210> SEQ ID NO: 5

195 <211> LENGTH: 68

197 <212> TYPE: DNA

199 <213> ORGANISM: Candida antarctica

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204 atgggaattc catcatcatc atcatcacag cagcggccta ccttcggtt cggaccctgc      60
206 ctattcgc                                                                68
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211 <211> LENGTH: 24
213 <212> TYPE: DNA
215 <213> ORGANISM: Candida antarctica
219 <400> SEQUENCE: 6
220 cgactcgaac tacatcccc tctc                                          24
223 <210> SEQ ID NO: 7
225 <211> LENGTH: 24
227 <212> TYPE: DNA
229 <213> ORGANISM: Candida antarctica
233 <400> SEQUENCE: 7
234 gagaggggga tgtagttcga gtcg                                          24
237 <210> SEQ ID NO: 8
239 <211> LENGTH: 25
241 <212> TYPE: DNA
243 <213> ORGANISM: Candida antarctica
247 <400> SEQUENCE: 8
248 ggggtctgacc tacttccccca gtatc                                       25
251 <210> SEQ ID NO: 9
253 <211> LENGTH: 25
255 <212> TYPE: DNA
257 <213> ORGANISM: Candida antarctica
261 <400> SEQUENCE: 9
262 gatactgggg aagtaggtca gaccc                                         25
265 <210> SEQ ID NO: 10
267 <211> LENGTH: 21
269 <212> TYPE: DNA
271 <213> ORGANISM: Candida antarctica
275 <400> SEQUENCE: 10
276 cgatgagatt tccttcaatt t                                             21
279 <210> SEQ ID NO: 11
281 <211> LENGTH: 21
283 <212> TYPE: DNA
285 <213> ORGANISM: Candida antarctica
289 <400> SEQUENCE: 11
290 tctagaaagg tggcggccgc c                                             21
293 <210> SEQ ID NO: 12
295 <211> LENGTH: 22
297 <212> TYPE: DNA
299 <213> ORGANISM: Candida antarctica
303 <400> SEQUENCE: 12
304 gaagctggat tccatcatca tc                                           22
307 <210> SEQ ID NO: 13
309 <211> LENGTH: 21
311 <212> TYPE: DNA
313 <213> ORGANISM: Candida antarctica

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317 <400> SEQUENCE: 13
318 tctagaaagg tggcggccgc c 21
321 <210> SEQ ID NO: 14
323 <211> LENGTH: 1074
325 <212> TYPE: DNA
327 <213> ORGANISM: Bacillus subtilis
331 <400> SEQUENCE: 14
332 atgtctgtgc aggctgccgg aaaaagcagt acagaaaaga aatacattgt cggattttaa 60
334 cagacaatga gtgccatgag ttccgccaaag aaaaaggatg ttatttctga aaaaggcgga 120
336 aaggttcaaa agcaatttaa gtatgttaac gcggccgcag caacattgga tgaaaaagct 180
338 gtaaaagaat tgaaaaaaga tccgagcggt gcatatgtgg aagaagatca tattgcacat 240
340 gaatatgcgc aatctgttcc ttatggcatt tctcaaatta aagcgccggc tcttcactct 300
342 caaggctaca caggctctaa cgtaaaagta gctgttatcg acagcggaat tgactcttct 360
344 catcctgact taaacgtcag aggcggagca agcttcgtac cttctgaaac aaaccatac 420
346 caggacggca gttctcacgg tacgcatgta gccggtacga ttgccgctct taataactca 480
348 atcgggtgtt tgggcgttag cccaagcgca tcattatatg cagtaaaagt gcttgattca 540
350 acaggaagcg gccaatatag ctggattatt aacggcattg agtgggccat ttccaacaat 600
352 atggatgta tcaacatgag ccttggcgga cctactggtt ctacagcgct gaaaacagtc 660
354 gttgacaaaag ccgtttccag cggtatcgct gttgctgccg cagccggaaa cgaaggttca 720
356 tccggaagca caagcacagt cggctaccct gcaaaatata cttctactat tgcagtaggt 780
358 gcggtaaaaca gcagcaacca aagagcttca ttctocagcg caggttctga gcttgatgtg 840
360 atggctcctg gcgtgtccat ccaaagcaca ctctcgtggag gcacttacgg cgcttataac 900
362 ggaacgtcca tggcgactcc tcacgttgcc ggagcagcag cgtaattct ttctaagcac 960
364 ccgacttgga caaacgcgca agtccgtgat cgtttagaaa gcactgcaac atatcttgga 1020
366 aactctttct actatggaaa agggtaatac aacgtacaag cagctgcaca ataa 1074
369 <210> SEQ ID NO: 15
371 <211> LENGTH: 357
373 <212> TYPE: PRT
375 <213> ORGANISM: Bacillus subtilis
379 <400> SEQUENCE: 15
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382 1 5 10 15
384 Val Gly Phe Lys Gln Thr Met Ser Ala Met Ser Ser Ala Lys Lys Lys
385 20 25 30
387 Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Gln Phe Lys Tyr
388 35 40 45
390 Val Asn Ala Ala Ala Thr Leu Asp Glu Lys Ala Val Lys Glu Leu
391 50 55 60
393 Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His Ile Ala His
394 65 70 75 80
396 Glu Tyr Ala Gln Ser Val Pro Tyr Gly Ile Ser Gln Ile Lys Ala Pro
397 85 90 95
399 Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val
400 100 105 110
402 Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Asn Val Arg Gly
403 115 120 125
405 Gly Ala Ser Phe Val Pro Ser Glu Thr Asn Pro Tyr Gln Asp Gly Ser
406 130 135 140
408 Ser His Gly Thr His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser

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409 145          150          155          160
411 Ile Gly Val Leu Gly Val Ser Pro Ser Ala Ser Leu Tyr Ala Val Lys
412          165          170          175
414 Val Leu Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly
415          180          185          190
417 Ile Glu Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu
418          195          200          205
420 Gly Gly Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala
421          210          215          220
423 Val Ser Ser Gly Ile Val Val Ala Ala Ala Gly Asn Glu Gly Ser
424 225          230          235          240
426 Ser Gly Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr
427          245          250          255
429 Ile Ala Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala Ser Phe Ser
430          260          265          270
432 Ser Ala Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln
433          275          280          285
435 Ser Thr Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Ser Met
436          290          295          300
438 Ala Thr Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His
439 305          310          315          320
441 Pro Thr Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala
442          325          330          335
444 Thr Tyr Leu Gly Asn Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val
445          340          345          350
447 Gln Ala Ala Ala Gln
448          355
450 <210> SEQ ID NO: 16
452 <211> LENGTH: 269
454 <212> TYPE: PRT
456 <213> ORGANISM: Bacillus subtilis
460 <400> SEQUENCE: 16
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463 1          5          10          15
465 His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
466          20          25          30
468 Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
469          35          40          45
471 Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
472          50          55          60
474 His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
475 65          70          75          80
477 Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
478          85          90          95
480 Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
481          100          105          110
483 Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
484          115          120          125
486 Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly

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VERIFICATION SUMMARY

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